

REMARKS/ARGUMENTS

This is in response to the Official Action mailed July 23, 2009 for the above-captioned application. Reconsideration of the application as amended is respectfully requested.

The Examiner asserts that claims 64-71 lack the special technical feature of the elected group I and therefore these claims are treated as non-elected. As previously pointed out, however, these claims are directed in part to subject matter that falls within the scope of elected claims. Notably, a construct according to many of these claims would fall within the scope of the elected construct claims, which are generic with respect to the elected invention. Accordingly, maintaining the restriction requirement could result in the issuance of two patents which would cover the same construct. Thus, reconsideration of newly imposed restriction requirement is requested.

The claims have been amended in view of the Examiner's remarks concerning informalities. Applicants have not amended claims 35 and 42, however, because these are not dependent claims.

The Examiner stated that there terms "MDH-like", "functionally active" and "shown in" are indefinite and rejected claims containing them under 35 USC § 112, second paragraph. Applicants have amended claim 30 to delete the term "MDH-like" and reference to fragments. Claim 31 has been amended to refer to full length DNA or its complement, antisense or corresponding RNA, and to variants of the full length DNA, complement or antisense that are functionally active and have at least approximately 95% identity to the starting sequence. Applicants point out that the term "functionally active" is defined in the specification in the paragraph bridging Pages 5 and 6. The SEQ ID Nos. are referred to without the statement "shown in."

The Examiner rejected claims 30, 31, 33, 35, and 40-42 as lacking written description. Based on the Examiner's statement of the claim interpretation to support the rejection, Applicants believe that the amendments presented fully address the rejection as directed to these claims. It is noted, however, that the Examiner's argument that the specification only describes a polynucleotide of seq ID No. 271 is not understood nor is it agreed to. The application discloses multiple MDH sequences from *Trifolium*. Thus, Applicants have disclosed multiple species within the scope of claim 30 and these are specifically identified in the sequences listed in other claims.

The Examiner rejected claims 30, 31, 33, 35, and 40-42 as lacking enablement. Based on the Examiner's statement of the claim interpretation to support the rejection, Applicants believe that the amendments presented fully address the rejection as directed to these claims. The functional activity is MDH activity, which is the activity of the sequences listed.

Claims 30, 33, 35, and 40-42 stand rejected as anticipated by Tesfaye et al. Claims 30, 31, 33 and 35 are rejected as anticipated by Ellison et al. The Examiner has not identified any specific sequence as anticipatory, but rather has relied on the generalized statements about the broad scope of the claims as interpreted. This is not sufficient to create a prima facie case of anticipation, not does it facilitate a meaningful response.

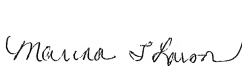
In the case of Tesfaye, the reference does disclose an MDH enzyme, but it is from alfalfa, not clover. The nucleic acid sequence of this enzyme does not fall within the scope of the present claims as it is different by more than 5 % for all sequences (See ex. A, Columns for AF020273).

In the case of Ellison, the reference discloses an alcohol dehydrogenase not an MDH, albeit from clover. In this case, the greatest nucleotide commonality is less than 50% and there is little or no sequence similarity at the protein level. (See ex. A, Columns for X14826).

Thus, Applicants submit that neither of these references is anticipatory, and the rejections should be withdrawn.

In view of the foregoing, Applicants submit that this application is in form for allowance, and such action is respectfully urged.

Respectfully submitted,

A handwritten signature in cursive script, reading "Marina T. Larson".

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attachment

Exhibit A

Table: Sequence identity between TrMDH nucleotide and protein sequence with X14826 and AF020273 nucleotide and protein sequences.

	Nucl. Seq ID No.	Tesfaye AF020273		Ellison X14826	
		nucleotide	protein	nucleotide	protein
TrMDHa	205	48.8	21.5	46.2	11.4
TrMDHb	218	47.0	17.5	46.7	12.3
TrMDHc	252	57.4	54.8	44.9	12.4
TrMDHd	271	91.4	90.5	48.1	15.3
TrMDHe	276	58.7	51.4	43.8	15.3
TrMDHf	288	59.7	52.4	46.8	16.5
TrMDHg	293	48.7	16.8	48.6	11.3
TrMDHh	297	59.7	52.2	46.8	16.4
TrMDHi	302	46.6	11.7	45.3	9.8
TrMDHj	306	46.9	17.1	46.9	10.7
TrMDHk	308	46.8	12.2	46.8	16.3